

XX



Dh	1861	aatttttttgttatcttcacggagagacaanaagttaatacatgttggccacagctgtrttt	1920
Oy	1921	gaactctgactcaaaagtatctggccacccttggccctccaaagtcttggagttacaggt	1980
Dh	1921	gaactcttguaaccacaaagtgatctggccacccttggccctccaaagtcttggagttacaggt	1980
Oy	1981	gaagccacttgcgcacgcagcttcaatgcactttaaacaatataaacaactttccataaaa	2040
Dh	1981	gaagccacttgcgcacgcagcttcaatgcactttaaacaatataaacaactttccataaaa	2040
Oy	2041	aagtttcaaataggttatcttcaaaaaaatttvgltagagaacatvgaaagctttctgtac	2100
Dh	2041	aagtttcaaataggttatcttcaaaaaaatttvgltagagaacatvgaaagctttctgtac	2100
Oy	2101	atacactcaaatagaatgcgcaaaaatttvgagacaatatttaagttttcaaaagct	2160
Dh	2101	atacactcaaatagaatgcgcaaaaatttvgagacaatatttaagttttcaaaagct	2160
Oy	2161	gaaaaagtgltaatvgaggggacgtgtaaatvgtgcaagccacttggaaaacaagatgag	2220
Dh	2161	gaaaaagtgltaatvgaggggacgtgtaaatvgtgcaagccacttggaaaacaagatgag	2220
Oy	2221	gatttctcaaaaaaagaattacgcaataatccacgaatbccaatctgcgatataacca	2280
Dh	2221	gatttctcaaaaaaagaattacgcaataatccacgaatbccaatctgcgatataacca	2280
Oy	2281	caagagcttgaagccgggaacttaagcaatgttatcaatcatgcttcaacagagaatca	2340
Dh	2281	caagagcttgaagccgggaacttaagcaatgttatcaatcatgcttcaacagagaatca	2340
Oy	2341	ttcatactagccaagaatvggtvggcagcccccggttcatttgaatagatvgaaatgaaac	2400
Dh	2341	ttcatactagccaagaatvggtvggcagcccccggttcatttgaatagatvgaaatgaaac	2400
Oy	2401	aacacaacacatgaaatgttatccacttaaaagtacagacacagagatgaaacttggagcca	2460
Dh	2401	aacacaacacatgaaatgttatccacttaaaagtacagacacagagatgaaacttggagcca	2460
Oy	2461	tttatactaatgaaatatbaccagcttcaacgagaagaaagatctctctgttatagaaatacag	2520
Dh	2461	tttatactaatgaaatatbaccagcttcaacgagaagaaagatctctctgttatagaaatacag	2520
Oy	2521	agtggtctcatctcaataaagtvgaaatvgatgagtcgcaagggtcttggaggaatgcagaaatg	2580
Dh	2521	agtggtctcatctcaataaagtvgaaatvgatgagtcgcaagggtcttggaggaatgcagaaatg	2580
Oy	2581	gaagtttaatggtttaaacacaggtacaggggtctcaagtttvggaaataaaaaagttctvgag	2640
Dh	2581	gaagtttaatggtttaaacacaggtacaggggtctcaagtttvggaaataaaaaagttctvgag	2640
Oy	2641	tgagtaggtgcgagacggtttccaaatgtcaatgacacttaatgcccacaacatgtactcttaa	2700
Dh	2641	tgagtaggtgcgagacggtttccaaatgtcaatgacacttaatgcccacaacatgtactcttaa	2700
Oy	2701	aaacagtgaaacggcgacgggtggtctcaagcgttaatcccaagacttttggggagacaaggg	2760
Dh	2701	aaacagtgaaacggcgacgggtggtctcaagcgttaatcccaagacttttggggagacaaggg	2760
Oy	2761	ggggcgagtaacaaagttcaggaagatacgaagccatctgtgctaaacaggtgaaaccccgctt	2820
Dh	2761	ggggcgagtaacaaagttcaggaagatacgaagccatctgtgctaaacaggtgaaaccccgctt	2820
Oy	2821	ctactcaaaaaatacaaaaataattacgcgggttgcgttgcgggcgtctgtatgtccagctaac	2880
Dh	2821	ctactcaaaaaatacaaaaataattacgcgggttgcgttgcgggcgtctgtatgtccagctaac	2880
Oy	2881	tcgggggggtctgagagcaaggaagatvggttggaacatvgggagggcgaggtcttgcagtgagctg	2940
Dh	2881	tcgggggggtctgagagcaaggaagatvggttggaacatvgggagggcgaggtcttgcagtgagctg	2940
Oy	2941	gattccacacatgcactcaagcttggcgagacagagaagatccggtctcaaaacaacaa	3000

Dh	2941	gacacagccactgcatccacagcctcgycagcagcgaagactcgtcccaacaaacaa	300
Oy	3001	agccaaacaaacaaacaggttaaaattttttttttttaagatcacgycgaaataga	3060
Dh	3001	agccaaacaaacaaacaggttaaaattttttttttttaagatcacgycgaaataga	3060
Oy	3061	atgagatcttaacaaatactgacagcgggtgggaagaggaactactagaatatttt	3120
Dh	3061	atgagatcttaacaaatactgacagcgggtgggaagaggaactactagaatatttt	3120
Oy	3121	ttccocctcttcttaacaaatagatcgatgcttaagggtgggaatagaactccctggcg	3180
Dh	3121	ttccocctcttcttaacaaatagatcgatgcttaagggtgggaatagaactccctggcg	3180
Oy	3181	agccatcttaagcaagaatcacagccactttctcttaagagatctgatagtcaaacattt	3240
Dh	3181	agccatcttaagcaagaatcacagccactttctcttaagagatctgatagtcaaacattt	3240
Oy	3241	ccacttgagagctatgctctgcagctaccagctctgcttgagcgttgcaaaagcgc	3300
Dh	3241	ccacttgagagctatgctctgcagctaccagctctgcttgagcgttgcaaaagcgc	3300
Oy	3301	aaagcgaacgctaaaggaatgacgcgaagagagccttagttatttaacataaagctta	3360
Dh	3301	aaagcgaacgctaaaggaatgacgcgaagagagccttagttatttaacataaagctta	3360
Oy	3361	tgcgaagagagatgcgaagccaaactatgttgctgatactcgcatacctacagtcagaataca	3420
Dh	3361	tgcgaagagagatgcgaagccaaactatgttgctgatactcgcatacctacagtcagaataca	3420
Oy	3421	cagagaaaggagagatttgcgcgtataatttaaatctcttccttgcaaaagcagtcac	3480
Dh	3421	cagagaaaggagagatttgcgcgtataatttaaatctcttccttgcaaaagcagtcac	3480
Oy	3481	aaaaaagtgagagcaacaaactggaacaaatattcacacagctcgtatgttagaagc	3540
Dh	3481	aaaaaagtgagagcaacaaactggaacaaatattcacacagctcgtatgttagaagc	3540
Oy	3541	actatattcttaattcaaaaagacatttaccacaaagaagacaaataactagaat	3600
Dh	3541	actatattcttaattcaaaaagacatttaccacaaagaagacaaataactagaat	3600
Oy	3601	tgcgcaaaagacttccatttgcctgacataacgtaggaagccttggtttaacttccca	3660
Dh	3601	tgcgcaaaagacttccatttgcctgacataacgtaggaagccttggtttaacttccca	3660
Oy	3661	tcattcttcaacttcacagaccagcctaatttgcatttatttattatagatattat	3720
Dh	3661	tcattcttcaacttcacagaccagcctaatttgcatttatttattatagatattat	3720
Oy	3721	ttagagacagagctcttgccctgcctcccaagcgcgagcgcgagtcgatacgtgacatagctaac	3780
Dh	3721	ttagagacagagctcttgccctgcctcccaagcgcgagcgcgagtcgatacgtgacatagctaac	3780
Oy	3781	aacagcctactactcccggttcaagaatactctcaactctagcttcccgagtagcttg	3840
Dh	3781	aacagcctactactcccggttcaagaatactctcaactctagcttcccgagtagcttg	3840
Oy	3841	actgtaggcacatgcacacatgcccagctaaattttatttcttgtagagcagaagccc	3900
Dh	3841	actgtaggcacatgcacacatgcccagctaaattttatttcttgtagagcagaagccc	3900
Oy	3901	attaatgctgcgagagctgctctgaactcgtgcttcacagcagatctccctcgtgct	3960
Dh	3901	attaatgctgcgagagctgctctgaactcgtgcttcacagcagatctccctcgtgct	3960
Oy	3961	cccaaaagtgtggatttaagagcataagcaactgcctccagccttatttcgatatattac	4020
Dh	3961	cccaaaagtgtggatttaagagcataagcaactgcctccagccttatttcgatatattac	4020
Oy	4021	tataaagtgtggaagtgatgatacgaactgcataataatttgcgcggaatactacac	4080
Dh	4021	tataaagtgtggaagtgatgatacgaactgcataataatttgcgcggaatactacac	4080





This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g. A28287035-2870355) are useful for DNA amplification and detection methods. RBP-7 alleles markers (see A28286993-287034) are useful for diagnosis of regions related to alteration in the regulation or in the coding regions of RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include thyroid hyperplasia, psoriasis, benign prostatic hypertrophy, cancers including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukemias, and lymphomas. RBP-7 antibodies are useful as diagnostic agents.

Qy	1747	ggaggtgcaactggtg----tga	tggtgccaactgtgaacctccacctccagagctcaagtga	1803
Db	80256	GGAGTGCATGSGCGGCAATGATCATTTCTCTACTGTGAGCTTAACTCCTCGGAGTCAAGATGA		8019
Qy	1804	ttctcatgctctcaagctccctccagtagcttgattacaaggcgaatttttttllacaat	1863	
Db	80196	TCTCTTCAACCTTACCTCCACAGTACGTAGTACGACACAGGTGTCACACTATCACACCGACT	8013	
Qy	1864	tttttttgtaatttccagagagacaaaagcttaacatgctgggacaggttggttttaa	1923	
Db	80136	AATTTTTGTTTTTGTGTGAGATG----GGGTTTTGCAAGTGTGTCCAGCTGGTCTCCAA	8008	
Qy	1924	ctctcgacctaaagttagtctgcccacgtcttgctcccaagtctggattacag---tg	1981	
Db	80080	CTCTGGGGCTTAACCCATCTGTGCCCACTCGGCTCCCAACACTGCTGGATTCADGGCTG	80021	
Qy	1982	agccacctcgccagccagttcactgaccttaaacata-aaacatttccaa	2040	
Db	80020	AGCCACCAACCCACCCCGGAAATCTGTAGCTGTGCTCTGCTCACTTACCTCATGTGTA	79961	
Qy	2041	aagttcaaatggtatttcaaaaaagtgtggtgagagacatgaaagcttctctac	2100	
Db	79960	TTTTATATATCTGAAATATATATTTTGTGTAATCTGTATACATATAGATTTACTTAA	79901	
Qy	2101	ataacac------aataagcatgcaaaatgtgtgagcaaatlttaagtttcaaa	2155	
Db	79900	TGACTTTTITTTGGTAAACGGGAAATTAATTCGGATTCACCTTTTGCAAGCAAA	79841	
Qy	2156	agccctgaaagtgcttaatgtagggccactgtataaigtgcgcacatgtgaaacag	2215	
Db	79840	CAGATGATTAATTAATGTATGTCTCCACACCGAAATTAAGGTGTGCTCTTTAAAGCAGA	79781	
Qy	2216	atgagagatttctcaaaaaagaaatlaagcatcaacccagcaatgcacatctcgata-	2274	
Db	79780	AAAA-----TAAAGAGAGAGAGAGATTTATACACAGTGATTTCTATTTTAAG	79728	
Qy	2275	taccacaagaacgtcgaagccggaacttaagatgtattcatcatcaatgttccaagaa	2334	
Db	79727	TATCTGTATCTTTTCACTTGTCTCAACGAAAGAAATTTCTAAGAGTTGTTTA---A	79672	
Qy	2335	gtatcatcttactagccaaaagtggtgcagccccgtlccatttatagatgaatg	2394	
Db	79671	GAATCACAATATAGTAAATTTTCAANTAAAGACACAGTCTCTCCATGACATFACAA	79612	
Qy	2395	gtaaacaacaacaacatgaagatcatcacccctaaagaatcaagacacaggtgaactg	2454	
Db	79611	AGAAACATAGGCAATATCTGTGTCCTATATCTCATATGTCAGAAAGTAGGGGCACTGTGG	79552	
Qy	2455	gaagcattactaactaaatgtgcacgaatgaagaaagacagatctctgtatgaatg	2514	
Db	79551	TTTTCAAGGGCATMAAAAGACCTGGGGGTAGGGTGAATTTGTCCATTAAGACTTAAAG	79492	
Qy	2515	actcagatggtgtccatcatcaataagtgaatgtagctgcagaggggtctgaaggagtcga	2574	
Db	79491	AGCAAAACCAAGAGGCTCTGAAAGAGTGATTTAAAGGCACATAGAAACCTCCGATGGCT	79432	
Qy	2575	gagttgggaagttaagtgtatgaacagtgacggagtcctcagtttgggaagataaagatc	2634	
Db	79431	AGAGGGAATAATGTCTATGGCCCTGTACCTTAAATGGCGTCGAGAAATATGAACTGGG	79372	
Qy	2635	tggaggtgtgataagccgaaggttccacaatgtcaatgaatgaatgaatgaatgaatga	2694	
Db	79371	ATTTTACCTTAACTTCTTATGAGATTTTAAATGTGACATATGTAAATACAAAGAAAGATAC	79312	
Qy	2695	tcttaaaaacagttgacccgagacaggtgtgtcacaagctgt-aatccagacattggggga	2753	
Db	79311	C-----AGATATTTGGCTGGGGCGGTGGCTCACGGCTTATCCAGCACTTTGGGAGG	79257	
Qy	2754	ccgagccgagccgagataca--ggtgcagagatctggagacctctctgctcaaacgtgaa	2811	
Db	79256	CCAAAGTGGGGGATCACTTGAAGGCTAGAGGTTTCAAGACCAACCTGGCAACATGTGGCAA	79197	





PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Becerra SP, Chader GJ, Schwartz JP, Tanikawa T;

XX WPI: 1996-03966/04.

DR P-PSDB: AAR90287.

XX Use of pigment epithelium derived factor - for enhancing neuronal  
PT cell survival and inhibiting glial cell proliferation, useful, e.g.  
PT In CNS cell culture or to treat neuro-degenerative diseases

PS Disclosure: Page 100-122; 151pp; English.

XX Pigment epithelium-derived factor (PEDF) has both neurotrophic and  
CC glial-static activity, making it useful in cases where neurons die  
CC quickly and glia tend to proliferate (gliosis), e.g. in CNS cell  
CC culture, in neurodegenerative diseases and in CNS injury. The  
CC neurotrophic effect of PEDF is especially useful for enhancing  
CC survival of neuronal cell cultures intended for use in  
CC transplantation. These include cultures of human foetal brain cells  
CC and neural retina and photoreceptor cells. The glial-static activity  
CC of PEDF can be applied to inhibiting glial cell proliferation in  
CC certain tumors. Antibodies directed against PEDF can be used for  
CC inhibiting PEDF activity or in an immunoassay for determining  
CC levels of PEDF in fluid, cellular or tissue samples e.g for  
CC determining ageing and/or other degenerative diseases.

XX Sequence 22481 BP; 5280 A; 5708 C; 6136 G; 5347 T; 10 other;

Query Match 5.5%; Score 357.6; DB 17; Length 22481;  
Best Local Similarity 76.8%; Pred. No. 2.9e-69;

Matches 490; Conservative 0; Mismatches 139; Indels 9; Gaps 4;

QY 1347 ccgagatttaaaatgacattagagctggcgagctgctcagctgtaaccagca 1406  
DB 12796 caggagattaaagctgagtgagggcgagctgctcagctgtaaccagca 12855  
QY 1407 cttggagagcgccagatgagctacagagatcagagacccacttaaccac 1466  
DB 12856 cttggagagctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 12915  
QY 1467 atggag 1526  
DB 12916 acggatgaacccgctcctactaaataaataaataaataaataaataaata 12975  
QY 1527 ctgtagtcacagctactcggagagctgagagcagagagagagagagagagag 1586  
DB 12976 ctgtagtcacagctactcggagagctgagagcagagagagagagagagag 13035  
QY 1587 gctgtgtagtgaagcagagatgcacacactcactcagagctggtgagagagag 1646  
DB 13036 ggttcag 13095  
QY 1647 gtcccaaaaaaaataaataaataaataaataaataaataaataaataaata 1706  
DB 13096 gtcccaaaaaaaataaataaataaataaataaataaataaataaataaata 13152  
QY 1707 gttgt 1763  
DB 13153 cttctgt 13212  
QY 1764 tgt 1823  
DB 13213 tctgt 13272  
QY 1824 gagtaagtagttagttagttagttagttagttagttagttagttagttagttag 1881  
DB 13273 aataagtagttagttagttagttagttagttagttagttagttagttagttag 13332  
QY 1882 gat 1941  
DB 13333 tagaga-tggggcctccacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 13391

QY 1942 ctgcccaccttggtctcccaagatgctgggattacaagg 1979  
DB 13392 ccattcttcgtgctgagcagagagagagagagagagagagagagagagag 13429

RESULT 6  
AAH18348/C  
ID AAH18348 standard; cDNA; 2073 BP.  
XX

AC AAH18348;

DT 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:18377.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

XX Claim 8; SEQ ID 18377; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC oligonucleotide which comprises at least 15 nucleotides, where the  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any special methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 2073 BP; 536 A; 501 C; 447 G; 589 T; 0 other;

Query Match 5.5%; Score 354.8; DB 22; Length 2073;











DD 1403 / ggLygaLcAcLgagyaLcCyayLcLyayuaLcAcLcyuLcuaLcayLyuaLcLc

14637 ggtgqatcacttgatgacgagtttgagacatactggccaacatgtgaaacc







FT	/number= "5"
FT	Intron
FT	/tag= "k"
FT	/number= "5"
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FT	/tag= "ah"
FT	/number= "17"





[illegible]

OY	1859	ttaaatttttttggtaatttttcaggagagaaacaaagttaaacaagctgagcgctgatt	1918
Db	12445	cagctaattt---taattttttgtagagatgagggtctctcaactatggttcgcagcgctgctc	12501
OY	1919	ttgaactctgactccaagatgactctgcccactctgtgctcccaagtctcgttgattacag	1978
Db	12502	tcagaactctggtgtctcaagcagatgcctcccaactctgtgctccaaagtctgtgtctacag	12561
OY	1979	-gtgagccactctgcgcgcgcgcacattcaactgacactttaaacataataacatttccaa	2037
Db	12562	tgtaggcacgagccagccagcc---ttgctgcacactggtgtagtatttactatgycacag	12618
OY	2038	aaaaagttcaaataggtattttcaaaaaattgttgtagagaaacttgaaagctttctct	2097
Db	12619	gcactgtcctatctctccctgtcgtgaatcccaaatgactctcaagacaaagctgactatt	12678
OY	2098	tacatacctaataaataagcaltgcataaaatctgtgtagcaaatattttagttttccaag	2157
Db	12679	atttccacttttccaatgta--gaanaactgtagaacacaaagatagtaataatttcccacag	12737
OY	2158	ccctgaaaaagtgtagtaatgtagagcactgttaaaatggtgtgcacactctgtgaaaaagagat	2217
Db	12738	tcatacagctagtagaagcaagagaggtgtgattttgaaaccaacttccacccaacagact	12797
OY	2218	gaggtatttccataaaaaaagaattaaagcattatccgacaaatgcacactctgtgataaac	2277
Db	12798	ttttgaaagtagaagcggaaagaggtctgtaggtactctctctgatactactgtttgaaac	12857
OY	2278	ccacaagactctgaagccggaacttaagcactgatactcaatacctatgttcaagcgtta	2337
Db	12858	atctgtggtccctttgtgacctctagactctgtgacctgtgtc-----	12866
OY	2338	tcactcaactagccaagaagtgtagtgccgcgcgcgcgtgtccattgtatagatgaatggtta	2397
Db	12897	-gttctctctcatcttcagcagatgtgtccatccctcagctcagactcagagccaaggtgaaaaagctc	12954
OY	2398	aacacacaaaacacatgaagtttcaaccccttaaaagtcagacaacaggtatanaactgtgag	2457
Db	12955	cccctcgaacagctgtcctttgcaagcactttaaagaataatccgttaacgtgtgcgtactacg	13014
OY	2458	ccattatacctaataatgaataatgtccagctcagcagaaagacagatctctctgtacagagttcct	2517
Db	13015	gagcttctcttaaatgtta-----cagagagagccagagaggtgtgtgtgtgtgtactag	13066
OY	2518	cagagtggtctcattatcaataaagtgtgaatgtgtgcctgcgcgaagggcctgtgaaagatctgaagta	2577
Db	13069	cagagtagctacatctctatgagccagagtttaaaaaggttggtagcagggacagcgtgtgtccctgc	13128
OY	2578	tgggaagttaattgtttgaacaagttacagagatcagatccagtttgggaagataaaaaagtctgcg	2637
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Fri Nov 30 11:03:15 2001

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Page 20

Db 13462 ccaagaccacgcccactgactccagcctggtgacagagcgcgagactctgtctcaaaaaa 13521  
Oy 2997 acaagcaaaacaaaaa 3013  
Db 13522 agaaaaataataaaaa 13538

Search completed: November 29, 2001, 09:34:35  
Job time: 19671 sec



us-09-526-329-40.rni

Page 1

OM nucleic - nucleic search, using sw model

(without alignments)  
7544.614 Million cell updates/sec

Sequence: 1 tctctctctccccctctc.....gttcattcagcagcagac 6486

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: /ann2 6/otodata/
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6: /cgn2_6/plodata/2/lna/5F_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	313.8	4.8	22481	5	PCT-US95-07201-43	Sequence 43, Appl
3	309.4	4.7	87350	3	US-08-781-891-79	Sequence 79, Appl
4	307.6	4.7	35060	3	US-08-814-095-7	Sequence 7, Appl
5	291.8	4.5	35060	3	US-08-814-095-7	Sequence 7, Appl
6	289.6	4.5	18073	4	US-09-078-924-12	Sequence 12, Appl
7	270	4.2	246240	2	US-08-724-94A-20	Sequence 20, Appl
8	270	4.2	246240	2	US-08-724-94A-20	Sequence 20, Appl
9	270	4.2	246240	2	US-08-724-94A-20	Sequence 22, Appl
10	268.2	4.1	3742.1	1	US-08-664-915-5	Sequence 5, Appl
11	268	4.1	3.20	1	US-08-629-939-5	Sequence 5, Appl
12	268	4.1	3.20	1	US-08-759-873-5	Sequence 5, Appl
13	264.6	4.1	14636	4	US-09-113-914-6	Sequence 6, Appl
14	263	4.1	14796	4	US-08-975-080-35	Sequence 35, Appl
15	263	4.1	1.4796	4	US-09-630-070-10	Sequence 10, Appl
16	258.6	4.0	176373	3	US-09-128-155-17	Sequence 17, Appl
17	257	4.0	4.517	5	PCT-US93-06251-83	Sequence 83, Appl
18	257	4.0	152331	3	US-09-128-155-16	Sequence 16, Appl
19	256.8	4.0	246240	2	US-08-724-94A-20	Sequence 20, Appl
20	256.8	4.0	246240	2	US-08-724-94A-20	Sequence 21, Appl
21	256.8	4.0	246240	2	US-08-724-94A-22	Sequence 22, Appl
22	256.4	4.0	246240	2	US-09-031-992-1	Sequence 1, Appl
23	256.4	4.0	2343	3	US-09-299-549-1	Sequence 1, Appl
24	256.4	4.0	87350	3	US-08-781-891-79	Sequence 79, Appl
25	255.6	3.9	176373	3	US-09-128-155-17	Sequence 17, Appl
26	255.4	3.9	13158	2	US-08-687-080-105	Sequence 105, Appl
27	255	3.9	588	4	US-09-385-982-128	Sequence 128, Appl

28	254.4	3.9	15328	2	US-08-888-697-33	Sequence 33, Appl
29	254.4	3.9	15328	5	PCR-US94.07926-33	Sequence 33, Appl
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44	249.4	3.8	6354	3	US-09-056-389A-12	Sequence 12, Appl
45	249.2	3.8	40328	3	US-08-742-105-102	Sequence 102, Appl

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ATTORNEY/AGENT INFORMATION:CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 2391.00066  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3506 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
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ANTI-SENSE: NO  
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Query Match 4.7%; Score 307.6; DB 3; Length 35060;
Best Local Similarity 48.6%; Pred. No. 5,6e-71;
Matches 1323; Conservative 0; Mismatches 1335; Indels 65; Gaps 15;

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RESULT 8  
US-08-724-394A-21

1 GENERAL INFORMATION:  
2 APPLICANT: Feder, John N.  
3 APPLICANT: Kronmoll, Gregory S.  
4 APPLICANT: Lauer, Peter M.  
5 APPLICANT: Ruddy, David A.  
6 APPLICANT: Thomas, Winston  
7 APPLICANT: Tsuchihashi, Zenta  
8 APPLICANT: Wolff, Roger K.  
9 TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
10 TITLE OF INVENTION: Sequences and Antibodies Thereo  
11 NUMBER OF SEQUENCES: 31  
12 CORRESPONDENCE ADDRESS:  
13

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5  COMPUTER: IBM PC compatible
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7  OPERATING SYSTEM: PC-DOS/MS-DOS
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9  SOFTWARE: Patentin Release #1.0, Version #1.30
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11 CURRENT APPLICATION DATA:
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13 APPLICATION NUMBER: US/08/724,394A
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15 FILING DATE: 01-Oct-1996

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US-08-724-394A-21

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Fri Nov 30 11:03:16 2001

us-09-526-329-40.rni

Page 13











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Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NHL19W, testis NHF, and B-cell  
NCL CGAP GC81) were mixed, and as circles were made *in*  
*vitro*. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297408-302087, 682632-687239,  
726608-728711, and 729096-731339. Subtraction by Bento  
Scorces and M. Estima Bonaldo "

**JOURNAL COMMENT**

Tagged Connectors  
Unpublished (1997)  
Contact: Mahindra GS, Zaackrone KD, Hood L  
University of Washington  
Seattle, WA 98195, USA  
Tel: (206) 616-8744  
Fax: (206) 685-7301  
Email: kzaackrone@u.washington.edu  
Sequence Tagged Connector  
Plate: CT 278 row: D column: 19  
Class: Bac ends  
High quality sequence, stop: 468.



REFERENCE 1 (bases 1 to 407)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 unknown library type  
 Insert Length: 675 Std Error: 0.00  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 383.  
 Location/Qualifiers  
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 /clone\_image="2000485"  
 /clone\_lib="NCI-CGAP\_Lym12"  
 /tissue\_type="Lymphoma, follicular mixed small and large cell"  
 /lab\_host="DH10B"  
 /note="Organ: Lymph node; Vector: PCMV-SPORT6; Site: 1; Salt: Site: 2; Not: Cloned unidirectionally. Primer: 01490 dt Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"  
 BASE COUNT 100 a 109 c 107 g 91 t  
 ORIGIN

Query Match 6.24; Score 403.4; DB 10; Length 407;  
 Best Local Similarity 99.84; Pred. No. 2.2e-39;  
 Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5929 ctatgctatcttcttgatgagcattcccaatcccttataccaccagagatgtgtc 5988  
 |||||||  
 DB 407 CTGATCTCTATCTTCTAGATGCCACCCAAATCCCTCATACCCACAGATGTGTC 348  
 QY 5989 ccagcagagcctccagcagcccccagtcagctgtgatttggaactcacatcgagcagc 6048  
 |||||||  
 DB 347 CCAGCCAGGCGCTCCAGCACCCCGAGTCGCTGATGTGGAACATCACATCGGAGGC 288  
 QY 6049 agtgggttggttgaagatgagatgaagggagccagctgtgattgtgactgtgagtc 6108  
 |||||||  
 DB 287 AGTGGTTCGGTTTAAAGATGAGATGAGGAGGAGCCAGTGTGATGTGAGATGTC 228  
 QY 6109 cctgtgtgatacagctgtgtgacacttggcccggaatagatccagtgctgagcagca 6168  
 |||||||  
 DB 227 CCGTGGGTATCAGTCTGCTGACACTTGGCCGAAATGATCCAGTGTGACAGCA 168  
 QY 6169 atgtacacggagcctgagtgagccatctgacagtgaggagcatgagggatgggttt 6228  
 |||||||  
 DB 167 ATGTACACCGAGCCTCAGTGAAGCCCATTTGACAGTGGAGACATGAGGATGGGTTT 108  
 QY 6229 ggcctgtgtctgtctattcaatccatcagcaggaaggagatgctagtcgtgaag 6288  
 |||||||  
 DB 107 GGCCTGTGCTTCTGCTTATTCAGTCCCTCAGCTACGGAAGGATCTAGTCCGTAAGG 48  
 QY 6289 tgaccacacagctgtgttaataacttattgtctacgtgtca 6333  
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 DB 47 TGACCTCACAGTACTGGTTAATTAACCTTATTTGCTCACTGTCAA 3

RESULT 9  
 AM292092 398 bp mRNA EST 16-JAN-2000  
 LOCUS UI-R-B12-agg-a-12-0-UI-s1 NCI CGAP\_Sub4 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2725559 3', mRNA sequence.  
 ACCESSION AM292092  
 VERSION AM292092.1 GI:6698728  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 398)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: [www.bio.lnlnl.gov/bbrp/image/image.html](http://www.bio.lnlnl.gov/bbrp/image/image.html)  
 Seq primer: M13 Forward  
 POLYA=yes.  
 Location/Qualifiers  
 1..398  
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 /db\_xref="taxon:9606"  
 /clone\_image="2725559"  
 /clone\_lib="NCI CGAP\_Sub4"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; The NCI CGAP\_Sub4 library is a subtracted library derived from the NCI CGAP\_Sub2 library which is a subtracted library derived from the NCI CGAP\_Sub1 library, which is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI CGAP libraries: NCI CGAP\_C04, NCI CGAP\_Pr22, NCI CGAP\_Lib28, NCI CGAP\_C010, NCI CGAP\_C016, NCI CGAP\_Kid5, NCI CGAP\_Kid12, NCI CGAP\_Kid3, NCI CGAP\_Kid11, NCI CGAP\_Lym2, NCI CGAP\_Br2, NCI CGAP\_C08, NCI CGAP\_C11, NCI CGAP\_Lel2, NCI CGAP\_Br23, NCI CGAP\_Lu5, NCI CGAP\_Lu24, NCI CGAP\_Lu19, NCI CGAP\_GC4, NCI CGAP\_GC6, NCI CGAP\_Br25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:  
 NCI CGAP\_Kid3 pool 1 : L1AM 3334-3337, 3687-3683, 3798-3803 (IMAGE Cloneds 132276-1123911, 1456008-1456775, 1500552-1502853) NCI CGAP\_Kid5 pool 1 : L1AM 3338-3342, 3722-3725, 3765-3778 (IMAGE Cloneds 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP\_Lu5 pool 1 : L1AM 3575-3582, 3851-3854 (IMAGE Cloneds 1414920-1417991, 1520904-1522439) NCI CGAP\_GC4 pool 1 : L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Cloneds 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP\_Pr22 pool 1 : L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneds 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP\_C010 pool 1 : L1AM 2644-2653, 2871-2872 (IMAGE Cloneds 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]  
 TAG\_LTB=NCI CGAP\_Lu5  
 TAG\_TISSUE=Lung  
 TAG\_SED=CANC

BASE COUNT 92 a 104 c 102 g 100 t  
 ORIGIN

Query Match 5.94; Score 379.8; DB 10; Length 398;  
 Best Local Similarity 99.58; Pred. No. 1.5e-36;  
 Matches 381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5951 cactcccaatcccttcataccacagagatgtgtgcccagcagcctccagcagccc 6010  
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 DB 398 CACTCCCAATCCCTTCATACCACAGAGATGTGTCACGACGAGCTCCAGCACCCC 339

QY 6011 caatgacgtcgtgatctggaactcaccatcgccagcgagtcgtggttaagaagatg 6070  
 |||||  
 DB 338 CAGTGCAGCTCGTGTGATGTGAATCAACATCGGAGCGAGTGTGTGGTTTAAGAGATGC 279  
 QY 6071 cattagaaggagccagctcgtgatctggaacttga tgcctctgggttaccatcttcgt 6130  
 |||||  
 DB 278 CATTACAGGAGCCAGCTCGATGTGAGCTTGATGCCCTGTGGTATCATTTCTGCTG 219  
 QY 6131 acacttggccggaatagatccagtcgtgagcaagaatgtaacccgagctcagatga 6190  
 |||||  
 DB 218 ACACCTTGGCGCCGAATAGATCCAGTCTGAGCAAGCAATGTACCGGAGCCTCAGTGA 159  
 QY 6191 gccacatcgacagtcggggagcaatgagggattggccctgtcttccttcattatca 6250  
 |||||  
 DB 158 GCCCATGTGCACAGTGGGAGACAGAGGATGGTTTGGCCTGTCTCTCTATTATCA 99  
 QY 6251 gtcctcagctcaggaaggatgctagtcgtgaaggtagcctcagctcagctgtaatt 6310  
 |||||  
 DB 98 GTCCCTACGCTCAGCGAAGGATGCTAGTCCGTGAAGGTGACCTACAGTGTGTTAAT 39  
 QY 6311 taactttatgtcactgtcca 6333  
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 DB 38 TAACTTTATGTCTCCTCTCA 16

RESULT 10  
 A1832007 376 bp mRNA EST 21-DEC-1999  
 A1832007/c wj99a02.x1 NCI\_CGAP\_Lym12 Homo sapiens cDNA clone IMAGE:2410922 3',  
 DEFINITION mRNA sequence.  
 A1832007  
 A1832007.1 GI:5452678  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 376)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Life Technologies catalog #: 11547-015  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrp/image/image.html  
 Insert Length: 1100 Std Error: 0.00  
 Seq primer: -400P from G1bco  
 High quality sequence stop: 375.  
 Location/Qualifiers

FEATURES  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:2410922"  
 /clone\_1ib="NCI\_CGAP\_Lym12"  
 /tissue\_type="lymphoma, follicular mixed small and large  
 cell"  
 /lab\_host="DH10B"  
 /note="Organ: lymph node; Vector: PCMV-SPORT6; site\_1:  
 Sail; site\_2: NotI; Cloned unidirectionally. Primer:  
 Oligo dT. Average insert size 1.25 kb. Life Technologies  
 catalog #: 11547-015"

BASE COUNT 92 a 105 c 97 g 82 t  
 ORIGIN

Query Match 5.8%; Score 373.4; DB 10; Length 376;  
 Best Local Similarity 99.7%; Pred. No. 8.9e-36;  
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5957 caaatcccttaataccaccagagatgltgccagccagcctccagcaccctcagtc 6016  
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 DB 376 CAAATCCCTCATACCCACAGAGATGTGTGCCAGCCAGCCTCCAGACCCCACTGC 317  
 QY 6017 agctcgtgttggaactcacaccatcgccagagatggttcgtttaaagaagatgcatag 6076  
 |||||  
 DB 316 AGCTCGTATTGGAACACTCACATCGGAGGAGTGTGCTTTAAGATGAGCATTAG 257  
 QY 6077 agggagccagctcgtgatgltgagatctgagtcgctgttggttaccatcttcagct 6136  
 |||||  
 DB 256 AGGAGCCAGCTCGATGTGAGTGTGATGATGCCCTGTGGGTATCACTCTGTCGACACTT 197  
 QY 6137 tggcccggaatagatccagtcgtcgaagcaatgtaaccggagcctcagctgagccat 6196  
 |||||  
 DB 196 TGCGCCCAATATGATTCACAGTCTGAGCAAGCAATGTACCGGAGCCTCAGTGAAGCCAT 137  
 QY 6197 ctgacagtcggggagcatggaaggatggttggccctgtcttcgtctatcagctcct 6256  
 |||||  
 DB 136 CTGCACAGTGGGAGCATGAGGAGGATGGCTTGGCCTGTCTCTCTATTATCACTCTT 77  
 QY 6257 cagctcaggaaggatgctagtcgtgaaggtagaagctcagctcagctgtaattaaact 6316  
 |||||  
 DB 76 CAGCTCAGCGAAGGATGCTAGTCCGTGAAGGTGACCTCACAGTGTGTTAATTA 17  
 QY 6317 ttattgtcactgtc 6331  
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 DB 16 TTATGTCTCCTCTCA 2

RESULT 11  
 A1250843 525 bp mRNA EST 21-DEC-1998  
 A1250843/c q10a04.x1 NCI\_CGAP\_Lym12 Homo sapiens cDNA clone IMAGE:2000910 3',  
 DEFINITION mRNA sequence.  
 A1250843  
 A1250843.1 GI:3847372  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 525)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 unknown library type  
 Insert Length: 1145 Std Error: 0.00  
 Seq primer: -400P from G1bco  
 High quality sequence stop: 336.  
 Location/Qualifiers

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /clone\_1ib="NCI\_CGAP\_Lym12"  
 /tissue\_type="lymphoma, follicular mixed small and large  
 cell"  
 /lab\_host="DH10B"  
 /note="Organ: lymph node; Vector: PCMV-SPORT6; site\_1:  
 Sail; site\_2: NotI; Cloned unidirectionally. Primer:  
 Oligo dT. Average insert size 1.25 kb. Life Technologies  
 catalog #: 11547-015"

BASE COUNT 143 a 141 c 136 g 104 t 1 others  
 ORIGIN

Query Match 5.7%; Score 371.8; DB 10; Length 525;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-35;  
 Matches 373; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy	5956	ccaaatccccttaacaccaccaagga	tgtgtcccaagcaggccccaagcccccaagt	6015
Db	377	CMAATCCCTTCATTACCCACAGNANTGTGTTGCCACCAGCAGCTTCAACACCCCAGAAGTG		
Oy	6016	cagctctgatttggaaactcaatccgcagcgacagtggttcggtttaagaagtgcatta		6075
Db	317	GAGCTCGTGAAWTGAACACTCAACATGGCGAGCGAGTGGTTCGCTTTAAGAAATGGCATTA		258
Oy	6076	gagggagcccaagctcuga	tgtggaacttgatagcctctggtgatcagtcttgtcaact	6135
Db	257	GAGGAGACCCAGCTCGAGTGTGGACTTTGGAGCCCTTGSGATCACTGACTGCTGCACACT		198
Oy	6136	ttggccccaataagattccagtgctcggcgagaagcaatgfaacccggagcctaagtgagacca		6195
Db	197	TTCGGCCGAATATGATCCAGTCTGAGCAAGCATATGACCCGAGCCTCAGTAGACCCA		138
Oy	6196	ttctgacaagtggggagcatlgaaggagttgggttgcctgtgctcttgcattaatcagctc		6255
Db	137	TCTGGACAAGTGGGAGCATGGAGGAGTGGCTTTGGCTTGCTTGCTTAATTCACCTCT		78
Oy	6256	loagctacaggaaggaatgcatagtccgtgaagtggaacctcaagtaacttggttaataac		6315
Db	77	TCAGCTCACGGAAGSAGTACGTCCGTGAGTGAGCGATCAAGTACAGTATGTTAATTAAC		18
Oy	6316	tttatgtctacgtc	6331	
Db	17	TTTTATTGCTCTACTGTC	2	
RESULT	12			
AOS18451				
LOCUS	AOS18451	457 bp	DNA	GSS
DEFINITION	HS_5101_A2_E10.SP66.RPCL-11 Human Male BAC Library Homo sapiens			05-MAY-1999
ACCESSION	AOS18451			
VERSION	AOS18451.1	GI:4743633		
KEYWORDS	GSS.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.			
	1 (bases 1 to 457)			
	Kellier,A., Shaker,R., Furlong,J., Young,J., Swartzell,S., Holzman,T.,			
	Hood,L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and			
JOURNAL	scanning the human genome			
MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)			
COMMENT	99380589			
	Contact: Mahindra GG, Wallace JC, Hood L			
	High Throughput Sequencing Center			
	University of Washington			
	401 Queen Anne Avenue North, Seattle, WA 98109, USA			
	Tel: (206) 616-3618			
	Fax: (206) 616-3887			
	Email: jwallace@u.washington.edu			
	Clones are derived from the human BAC library RPCL-11. For BAC			
	library availability, please contact Pieter de Jong			
	(piet@dejong.med.buffalo.edu). Clones may be purchased from			
	BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering_bac.htm">http://bacpac.med.buffalo.edu/ordering_bac.htm</a> )			
	or from Resear h Genetics ( <a href="http://inforesgen.com">inforesgen.com</a> ). BAC end Web Server:			
	<a href="http://www.hnsc.washington.edu">http://www.hnsc.washington.edu</a>			
	Plate: 677 row: I column: 20			
	Seq primer: SP6			
	Class: BAC ends			
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	/clone_id="RPCL-11 Human Male BAC Library"			
	/sex="male"			

		/note=Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
BASE COUNT	78 a 133 c 129 g 115 t	2 others
ORIGIN		
Query Match	5.4%; Score 348.2; DB 13;	Length 457;
Best Local Similarity	97.3%; Pred. No. 8.3e-33;	
Matches 364;	Conservative 0; Mismatches 9;	Indels 1; Gaps 1;
Oy 4330	tgaataacattacccttcacctgcgagaccactggccatgtcgtgqcgagccccagt	4389
Dd 1	TCATATACTTATTACTCTGTACCCTGGGAGCCACATGGGCATTTCTGTGGCAGCCCAATT	60
Oy 4390	ggcagggaaacccatcacatgatcttgcgcacctttcttgltcccttaaglatgaaccaag	4449
Dd 61	GGCAGGGAACCCATCATCATGATTTGGCCGCCCTCTTTCTTGTCGCCCTAGTAGAACCCAG	120
Oy 4450	catacaagtcactctgtgacagaatggcagatcatataccggagagctactctctccggcca	4509
Dd 121	CATCACAGTCACATTGTGGCGAATGGCAGTGCATACCCGGAGAGCTACTCTCTCCGGCCA	180
Oy 4510	gattgcccttcccacagctgcgcgcgctgtgacagctcatacccggaagaagtacagagc	4569
Dd 181	GATGGCCCTTCTCCACAGTCGCCGCCCTCGTGACACTCTTACCCCAGGAGAAATTCACAGC	240.
Oy 4570	aacgagattccagttctcttggaaatagacagacaatggccagagcaagtgtgtgtgtctcta	4629
Dd 241	AACGGATTTCCAGTTCTGGCAATPACAGACATGACGACGACGAGCAAGTGTGGTGTCTTA	300
Oy 4630	ggttaaagagaaagatggccctcgtagctccgttccgtctctctctgtgcccccttg	4689
Dd 301	TGTGAAGAACAAGAGGGGCCCTCGTGTGACTGGCSTGG-CCTCTCTCTTGTGTGCCCTGC	359
Oy 4690	cccccttgagggttc	4703
Dd 360	CCCCNTGGGGCTTC	373
RESULT 13		
AM003249/c	328 bp mRNA	EST 08-MAR-2000
LOCUS	w66408.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476070	3',
DEFINITION	mRNA sequence.	
ACCESSION	AM003249	
VERSION	AM003249.1 GI:5850165	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo-	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT	Tumor Gene Index	
	Unpublished (1997)	
	Contact: Robert Strassberg, Ph.D.	
	Email: c9ap@femail.nhl.gov	
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael	
	R. Emmert-Buck, M.D., Ph.D.	
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima	
	Bonaldo, Ph.D.	
	cDNA library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	clone distribution: NCI-CGAP clone distribution Information can be	
	found through the I.M.A.G.E. Consortium/LNL at:	
	www.bio.lnl.gov/bbrp/image/image.html	
	Insert Length: 384 Std Error: 0.00	
	Seq primer: -400P from Glenco.	
FEATURES	Location/Qualifiers	

## SOURCE

1. 328  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2476070"  
 /clone\_1db="NCI\_CGAP\_GC6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 84 a 95 c 73 g 76 t  
 ORIGIN

Query Match 4.7%; Score 307.2; DB 10; Length 328;  
 Best Local Similarity 98.8%; Pred. No. 7.7e-28;  
 Matches 320; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 6011 caatgcagctgattggaactcaccatcgagagcagtggtg-cttaagaatg 6069  
 DB 328 CAGTGCAGCTGCTGATTGGAACCTCACCATCGCAGCAGAGTGGTTTAAAGATG 269  
 QY 6070 gattagagagagccagctctgagatggaactgagccctggtgatatcagttcgt 6129  
 DB 268 GCATTAGAGGAGGCCAGTGTGATGTGACCTTGATGCCCTGTGATCATGTTGCT 209  
 QY 6130 gacacttggccgaaatagatcagctgctgagcaacatggaacccgagagctcagtr 6189  
 DB 208 GACACTTTGGCCCAATATAGATCAGTCTGAGCAACATGTACACCGAGCTCAGTG 149  
 QY 6190 accccatcgagagctgagagagatgagatggtttgagcttgccttccttcttattc 6249  
 DB 148 AGCCCATCTGCACAGTGGAGCAGTGGAGGATGGTTGGCTTGTCTTATTC 89  
 QY 6250 agtccctcagctcaggaagagatgctagctgagagtgagcccaacagactgtttaa 6309  
 DB 88 AGTCTTACGCTCAGGAGAGGATGCTAGTCCGTGAAGGAGACCTCCAGTACTGTTAA 29  
 QY 6310 ttaacttattgtcactgctca 6333  
 DB 28 TTAACCTTATTGCTCAGCTGCA 5

RESULT 14  
 AA825205/c 338 bp mRNA EST 21-APR-1998  
 LOCUS oc66e05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1354688 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AA825205  
 VERSION AA825205.1 GI:2898502  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 338)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cgapbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.

## FEATURES

## SOURCE

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILM at:  
 www.bio.illn.gov/dbp/image/image.html  
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 Seq primer: -40ml3 fwd. Et from Amersham  
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 Location/Qualifiers

1. 338  
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 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - Oligo(dT) primer [5'-TGTACCAATCTGACAGTGGAGCCGCTCATTTTTTTTTTTT-3'] 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 80 a 91 c 69 g 98 t  
 ORIGIN

Query Match 4.7%; Score 306.8; DB 10; Length 338;  
 Best Local Similarity 99.4%; Pred. No. 8.5e-28;  
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 338 GATTGAAACTCACACATCGCAGCAGTGTCTGTTAAGATGGATTACAGGAGAC 279  
 QY 6084 ccaagctgagatggaacttgatgacctgagtgatcaagctgctacacttgcccg 6143  
 DB 278 CCAAGCTGAGATGTGAGACTTGGATGCCCTGTGGGTATCACTTGTGTACACTTTGGCCG 219  
 QY 6144 aaatagatccagctgagcaagcaatgacacgagccctcagctgagccatctgacaa 6203  
 DB 218 AAATAGATCCAGTGTGAGCAGCAGATGTACACGAGCCTCATGATCTGACAA 159  
 QY 6204 gtggagagcagatgagagatggttgccctgctgcttcatcagctcagctca 6263  
 DB 158 GTGGAGACATGAGAGGATGGCTGTCTCTCTCTTATTCAGTCTTCAGCTCA 99  
 QY 6264 cggagagatgtagctcgtagagtgacccacagctgagtttaacttaacttattgc 6323  
 DB 98 CGGAAGGATGCTAGTCCCTGAGAGTACCTCAGTACTGCTTAATTAACCTTATTTC 39  
 QY 6324 tcaactgctca 6333  
 DB 38 TCACGTGCA 29

RESULT 15  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 315)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Life Technologies catalog #: 11547-015  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILMv at:  
[www-bio.ihl.gov/bhrp/image/image.html](http://www-bio.ihl.gov/bhrp/image/image.html)  
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BASE COUNT 82 a 94 c 70 g 69 t  
 ORIGIN

Query Match 4.7%; Score 304; DB 10; Length 315;  
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 DB 315 CAGCTCGTGAATGGAAACr-ACCATGGCAGGCAAGTTCGTTTAAGATGCACTTA 257  
 QY 6076 gaaggagccagctcgatgagctgagctgagctgagctgagctgagctgagct 6135  
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 DB 256 GAGGAGAGCCAGCTCGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 197  
 QY 6136 ttggccgaaatagatcagctgagcagcagcagcagcagcagcagcagcagcagcagc 6195  
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 DB 196 TTGGCCGAAATAGATCAGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 137  
 QY 6196 tctgcaagtgaggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6255  
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 DB 136 TCTGCACAGTGGGAGCATGAGGATGGGATGGGATGGGATGGGATGGGATGGGATGGG 77  
 QY 6256 tcagctcagcagaagagtgctagccgtgaagtgagcagcagcagcagcagcagcagc 6315  
 |||||||  
 DB 76 TCAGCTCAGCAGAGGAGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 17  
 QY 6316 ttattgtcactgtc 6331  
 |||||||  
 DB 16 TTTATTGTCTACTGTC 1

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